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AKV
RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/085,167

DATE: 03/19/2002
 TIME: 16:12:54

Input Set : A:\99-29C1.txt
 Output Set: N:\CRF3\03192002\J085167.raw

3 <110> APPLICANT: Holloway, James L.
 4 Lok, Si
 6 <120> TITLE OF INVENTION: SECRETED PROTEIN ZACRP4
 8 <130> FILE REFERENCE: 99-29
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/085,167
 C--> 10 <141> CURRENT FILING DATE: 2002-02-27
 10 <150> PRIOR APPLICATION NUMBER: 60/141,928
 11 <151> PRIOR FILING DATE: 1999-07-01
 14 <160> NUMBER OF SEQ ID NOS: 9
 16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1357
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (210)...(1196)
 27 <400> SEQUENCE: 1
 28 cggccggccc ctggcccccag caccctgtcc gctgccgcct cagagccggg aaaagcagcc 60
 29 ggagcccccgg cccgcctgc cgcagcgcgg gcggtcagcg cgcagccgg caccgcgc 120
 30 ctgcagccctg cagccgcag cccgcagccc ggagccagat cgcgggctca gaccgaaccc 180
 31 gactcgaccgg cccgcctccag ccaggcgcc atg ctg ccg ctt ctg ctg ggc ctg 233
 Met Leu Pro Leu Leu Leu Gly Leu
 32 1 5
 33 281
 35 ctg ggc cca gcg gcc tgc tgg gcc ctg ggc acc ccc ggc ccg gga
 36 Leu Gly Pro Ala Ala Cys Trp Ala Leu Gly Pro Thr Pro Gly Pro Gly
 37 10 15 20
 39 tcc tct gag ctg cgc tcg gcc ttc tcg gcg gca cgc acc acc ccc ctg 329
 40 Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg Thr Thr Pro Leu
 41 25 30 35 40
 43 gag ggc acg tcg gag atg gcg gtg acc ttc gac aag gtg tac gtg aac 377
 44 Glu Gly Thr Ser Glu Met Ala Val Thr Phe Asp Lys Val Tyr Val Asn
 45 45 50 55
 47 atc ggg ggc gac ttc gat gtg gcc acc ggc cag ttt cgc tgc cgc gtg 425
 48 Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe Arg Cys Arg Val
 49 60 65 70
 51 ccc ggc gcc tac ttc ttc tcc acg gct ggc aag gcc ccg cac aag 473
 52 Pro Gly Ala Tyr Phe Ser Phe Thr Ala Gly Lys Ala Pro His Lys
 53 75 80 85
 55 agc ctg tcg gtg atg ctg gtg cga aac cgc gac gag gtg cag ggc ctg
 56 Ser Leu Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala Leu
 57 90 95 100
 59 gcc ttc gac gag cag cgg cca ggc gcg cgg cgc gca gcc agc cag 569

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60	Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser Gln		
61	105 110 115 120		
63	agc gcc atg ctg cag ctc gac tac ggc gac aca gtc tgg ctg cgg ctg	617	
64	Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg Leu		
65	125 130 135		
67	cat ggc gcc ccg cac tac gcg cta ggc ggc ccc ggc gcc acc ttc agc	665	
68	His Gly Ala Pro His Tyr Ala Leu Gly Ala Pro Gly Ala Thr Phe Ser		
69	140 145 150		
71	ggc tac cta gtc tac gcc gac gac gtc gac gct gac ggc cct gcg cgc ggg	713	
72	Gly Tyr Leu Val Tyr Ala Asp Ala Asp Ala Asp Ala Pro Ala Arg Gly		
73	155 160 165		
75	ccg ccc gcg ccc ccc gag ccg cgc tcg gcc ttc tcg gcg gcg cgc acg	761	
76	Pro Pro Ala Pro Pro Glu Pro Arg Ser Ala Phe Ser Ala Ala Arg Thr		
77	170 175 180		
79	cgc agc ttg gtg ggc tcg gac gct ggc ccc ggg ccg cgg cac caa cca	809	
80	Arg Ser Leu Val Gly Ser Asp Ala Gly Pro Gly Pro Arg His Gln Pro		
81	185 190 195 200		
83	ctc gcc ttc gac acc gag ttc gtc aac att ggc ggc gac ttc gac gcg	857	
84	Leu Ala Phe Asp Thr Glu Phe Val Asn Ile Gly Gly Asp Phe Asp Ala		
85	205 210 215		
87	gcg gcc ggc gtg ttc cgc tgc cgt ctg ccc ggc gcc tac ttc ttc tcc	905	
88	Ala Ala Gly Val Phe Arg Cys Arg Leu Pro Gly Ala Tyr Phe Phe Ser		
89	220 225 230		
91	ttc acg ctg ggc aag ctg ccg cgt aag acg ctg tcg gtt aag ctg atg	953	
92	Phe Thr Leu Gly Lys Leu Pro Arg Lys Thr Leu Ser Val Lys Leu Met		
93	235 240 245		
95	aag aac cgc gac gag gtg cag gcc atg att tac gac gac ggc gcg tcg	1001	
96	Lys Asn Arg Asp Glu Val Gln Ala Met Ile Tyr Asp Asp Gly Ala Ser		
97	250 255 260		
99	ccg cgc cgc gag atg cag agc cag agc gtg atg ctg gcc ctg cgg cgc	1049	
100	Arg Arg Arg Glu Met Gln Ser Gln Ser Val Met Leu Ala Leu Arg Arg		
101	265 270 275 280		
103	ggc gac gcc gtc tgg ctg ctc agc cac gac cac gac ggc tac ggc gcc	1097	
104	Gly Asp Ala Val Trp Leu Leu Ser His Asp His Asp Gly Tyr Gly Ala		
105	285 290 295		
107	tac agc aac cac ggc aag tac atc acc ttc tcc ggc ttc ctg gtg tac	1145	
108	Tyr Ser Asn His Gly Lys Tyr Ile Thr Phe Ser Gly Phe Leu Val Tyr		
109	300 305 310		
111	ccc gac ctc gcc ccc gcc ccg ccg ggc ctc ggg gcc tcg gag cta	1193	
112	Pro Asp Leu Ala Pro Ala Ala Pro Pro Glu Leu Gly Ala Ser Glu Leu		
113	315 320 325		
115	ctg tgagccccgg gccagagaag agcccgaggag ggcaggggc gtgcatgcca	1246	
116	Leu		
118	ggccggggccc gaggtcgaa agtcccgccgc gagcgccacg gcctccgggc ggcctggac	1306	
119	tctgccaata aagcgaaag cggcacgca cagcgcccg cagcccaggc a	1357	
121	<210> SEQ ID NO: 2		
122	<211> LENGTH: 329		
123	<212> TYPE: PRT		
124	<213> ORGANISM: Homo sapiens		

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Input Set : A:\99-29C1.txt
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126 <400> SEQUENCE: 2
 127 Met Leu Pro Leu Leu Leu Gly Leu Leu Gly Pro Ala Ala Cys Trp Ala
 128 1 5 10 15
 129 Leu Gly Pro Thr Pro Gly Pro Gly Ser Ser Glu Leu Arg Ser Ala Phe
 130 20 25 30
 131 Ser Ala Ala Arg Thr Thr Pro Leu Glu Gly Thr Ser Glu Met Ala Val
 132 35 40 45
 133 Thr Phe Asp Lys Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala
 134 50 55 60
 135 Thr Gly Gln Phe Arg Cys Arg Val Pro Gly Ala Tyr Phe Phe Ser Phe
 136 65 70 75 80
 137 Thr Ala Gly Lys Ala Pro His Lys Ser Leu Ser Val Met Leu Val Arg
 138 85 90 95
 139 Asn Arg Asp Glu Val Gln Ala Leu Ala Phe Asp Glu Gln Arg Arg Pro
 140 100 105 110
 141 Gly Ala Arg Arg Ala Ala Ser Gln Ser Ala Met Leu Gln Leu Asp Tyr
 142 115 120 125
 143 Gly Asp Thr Val Trp Leu Arg Leu His Gly Ala Pro His Tyr Ala Leu
 144 130 135 140
 145 Gly Ala Pro Gly Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala
 146 145 150 155 160
 147 Asp Ala Asp Ala Pro Ala Arg Gly Pro Pro Ala Pro Pro Glu Pro Arg
 148 165 170 175
 149 Ser Ala Phe Ser Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala
 150 180 185 190
 151 Gly Pro Gly Pro Arg His Gln Pro Leu Ala Phe Asp Thr Glu Phe Val
 152 195 200 205
 153 Asn Ile Gly Gly Asp Phe Asp Ala Ala Ala Gly Val Phe Arg Cys Arg
 154 210 215 220
 155 Leu Pro Gly Ala Tyr Phe Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg
 156 225 230 235 240
 157 Lys Thr Leu Ser Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala
 158 245 250 255
 159 Met Ile Tyr Asp Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln
 160 260 265 270
 161 Ser Val Met Leu Ala Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser
 162 275 280 285
 163 His Asp His Asp Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile
 164 290 295 300
 165 Thr Phe Ser Gly Phe Leu Val Tyr Pro Asp Leu Ala Pro Ala Ala Pro
 166 305 310 315 320
 167 Pro Gly Leu Gly Ala Ser Glu Leu Leu
 168 325
 170 <210> SEQ ID NO: 3
 171 <211> LENGTH: 31
 172 <212> TYPE: PRT
 173 <213> ORGANISM: Artificial Sequence
 175 <220> FEATURE:
 176 <223> OTHER INFORMATION: C1q Aromatic Motif

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Input Set : A:\99-29C1.txt
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178 <221> NAME/KEY: VARIANT
179 <222> LOCATION: (2)...(6)
180 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
182 <221> NAME/KEY: VARIANT
183 <222> LOCATION: (7)...(7)
184 <223> OTHER INFORMATION: Xaa is asparagine or aspartic acid
186 <221> NAME/KEY: VARIANT
187 <222> LOCATION: (8)...(11)
188 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
190 <221> NAME/KEY: VARIANT
191 <222> LOCATION: (12)...(12)
192 <223> OTHER INFORMATION: Xaa is phenylalanine, tyrosine, tryptophan or
193 leucine
196 <221> NAME/KEY: VARIANT
197 <222> LOCATION: (13)...(18)
198 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
200 <221> NAME/KEY: VARIANT
201 <222> LOCATION: (20)...(24)
202 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
204 <221> NAME/KEY: VARIANT
205 <222> LOCATION: (26)...(26)
206 <223> OTHER INFORMATION: Xaa is any amino acid residue
208 <221> NAME/KEY: VARIANT
209 <222> LOCATION: (28)...(28)
210 <223> OTHER INFORMATION: Xaa is any amino acid residue
212 <221> NAME/KEY: VARIANT
213 <222> LOCATION: (30)...(30)
214 <223> OTHER INFORMATION: Xaa is any amino acid residue
216 <221> NAME/KEY: VARIANT
217 <222> LOCATION: (31)...(31)
218 <223> OTHER INFORMATION: Xaa is phenylalanine or tyrosine
220 <400> SEQUENCE: 3
W--> 221 Phe Xaa
222 1 5 10 15
W--> 223 Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa
224 20 25 30
226 <210> SEQ ID NO: 4
227 <211> LENGTH: 987
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Degenerate nucleotide sequence encoding the
233 polypeptide of SEQ ID NO:2
235 <221> NAME/KEY: variation
236 <222> LOCATION: (1)...(987)
237 <223> OTHER INFORMATION: Each N is A, T, G or C
239 <400> SEQUENCE: 4
W--> 240 atgytnccny tnytnytnng nytnytnngn ccngcngcnt gytggcnyt ngnccnacn 60
W--> 241 ccnggnccng gnwsnwsnga rytnmgnwsn gcnttywsng cngcnmgnac nacnccnytn 120

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W--> 242	garggnacnw sngaratggc ngtacntty gayaargtnt ayttnaayat hggngngay	180
W--> 243	ttygaygtng cnacngnca rttymgntgy mngntnccng gngcntaytt yttysntty	240
W--> 244	acngcnggna argncncna yaarwsnytn wsngtnatgy tngtnmgnmaa ymgngaygar	300
W--> 245	gtncargcny tngcnttyga ygarcarmgmgn mgnccnggng cnmgnmgnnc ngcnwsncar	360
W--> 246	wsngcnatgy tncarytna ytayggngay acngtntggy tnmgnytnc ayytngtnta yggngcncn	420
W--> 247	caytaygcn yngngcncc nngngcnacn ttywsngnt ayytngtnta ygcngaygcn	480
W--> 248	gaygcngayg cnccngcnmg ngnccncn gcncnccng arccnmgnws ngcnntywsn	540
W--> 249	gcngcnmgnna cnmgnwsnyt ngtnggnwsn gaygcnggn ncaycarccn	600
W--> 250	ytngcnttyg ayaacngartt ygttnaayath ggnngngayt tyaygcngc ngcngngtn	660
W--> 251	ttymgntgym gnytncngg ngcntaytty ttywsnttya cnytnggnnaa rytnccnmgn	720
W--> 252	aaracnytnw sngttnaayrt natgaaraay mgngaygarg tncargcnat gathaygay	780
W--> 253	gayggngcnw snmgnmgnmg ngaratgcar wsncarwsng tnatgytngc nytnmgnmgn	840
W--> 254	ggngaygcng tntggytnyt nwsncaygay caygayggnt ayggngccta ywsnaaycay	900
W--> 255	ggnaartaya thacnttyws ngnnttytn gtntayccng ayytngcncc ngcngcncn	960
W--> 256	ccnggnytng gngcnwsnga rytnytn	987
258	<210> SEQ ID NO: 5	
259	<211> LENGTH: 24	
260	<212> TYPE: DNA	
261	<213> ORGANISM: Artificial Sequence	
263	<220> FEATURE:	
264	<223> OTHER INFORMATION: Oligonucleotide ZC20,839	
266	<400> SEQUENCE: 5	24
267	atgtacttgc cgtgggttgcgt gtag	
269	<210> SEQ ID NO: 6	
270	<211> LENGTH: 23	
271	<212> TYPE: DNA	
272	<213> ORGANISM: Artificial Sequence	
274	<220> FEATURE:	
275	<223> OTHER INFORMATION: Oligonucleotide ZC20840	
277	<400> SEQUENCE: 6	23
278	cggacaccgag ttctgtcaaca ttg	
280	<210> SEQ ID NO: 7	
281	<211> LENGTH: 325	
282	<212> TYPE: DNA	
283	<213> ORGANISM: Artificial Sequence	
285	<220> FEATURE:	
286	<223> OTHER INFORMATION: Degenerate nucleotide sequence encoding the	
287	polypeptide of SEQ ID NO:2.	
289	<221> NAME/KEY: variation	
290	<222> LOCATION: (1)...(325)	
291	<223> OTHER INFORMATION: Each N is independently A, T, C or G.	
294	<400> SEQUENCE: 7	
295	ctggccccgg gccgcggcac caaccactcg cttcgacac cgagttcgac aacattggcg	60
W--> 296	gcgacttcga cggcgccggcc ggcgtgttcc gctgccgtct gnccggcgcc tacttcttct	120
W--> 297	ncttcacgct gggcaagctg cggcgtaaga cgctgtcggt taagctgatg aagaaccgcg	180
298	acgagggtca ggccatgatt tacgacgacg ggcgtcgcc ggcggcgag atgcagagcc	240
W--> 299	agagcgtat gctggccctg cggcgccggng acggcgctcg gctgtcagcc acgaccacga	300
300	cggtctacggc gcctacagca accac	325
302	<210> SEQ ID NO: 8	

VERIFICATION SUMMARY
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Input Set : A:\99-29C1.txt
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7